

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: MAERTENS, GEERT; STUYVER, LIEVEN;
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO

(ii) TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
ISOLATES

(iii) NUMBER OF SEQUENCES: 97

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: BIERMAN & MUSERLIAN
(B) STREET: 600 THIRD AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: USA
(F) ZIP: 10016

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/256,568
(B) FILING DATE: 18-JUL-1994
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/EP93/03325
(B) FILING DATE: 26-NOV-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP/93/402,129.6
(B) FILING DATE: 31-AUG-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP/92/403,222.0
(B) FILING DATE: 27-NOV-1992

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 19,683
(C) REFERENCE/DOCKET NUMBER: 410.004

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: YES
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME SEGMENT: HCV
 - (B) MAP POSITION: Position -299 of 5' end
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..27
 - (D) OTHER INFORMATION: /standard_name= "Universal HCV primer HcPr98"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCCTGTGAGG AACTWCTGTC TTCACGC

27

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: YES
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HCV (Okamoto et al., 1991)

(viii) POSITION IN GENOME:
(A) CHROMOSOME SEGMENT: HCV
(B) MAP POSITION: Position -1 of 5' end

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /standard_name= "Universal HCV primer HcPr29"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGTGCACGGT CTACGAGACC T

21

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: HCV

(viii) POSITION IN GENOME:
(A) CHROMOSOME SEGMENT: HCV
(B) MAP POSITION: Position -264 of 5' end

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..26
(D) OTHER INFORMATION: /standard_name= "Universal HCV primer HcPr95"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TCTAGCCATG GCGTTAGTRY GAGTGT

26

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: HCV

(B) MAP POSITION: Position -29 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..26

(D) OTHER INFORMATION: /standard_name= "Universal HCV primer HcPr96"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CACTCGCAAG CACCCTATCA GGCAGT

26

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 1 (Kato et al., 1990)

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: HCV type 1

(B) MAP POSITION: position -170 of the 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16
(D) OTHER INFORMATION: /standard_name= "HCV type 1 specific Probe HcPr124"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AATTGCCAGG ACGACC

16

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HCV type 1 (Kato et al., 1990)

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: HCV type 1
- (B) MAP POSITION: position -117 of 5'end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 1 specific Probe HcPr125"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TCTCCAGGCA TTGAGC

16

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 1b (Kato et al., 1990)

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: HCV type 1b

(B) MAP POSITION: position -103 of the 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type 1b specific Probe HcPr138"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CCGCGAGACT GCTAGC

16

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 2

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: HCV type 2

(B) MAP POSITION: position -83 of the 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type 2 specific Probe HcPr147"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TAGCGTTGGG TTGCGA

16

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HCV type 2a (Chan et al., 1992)

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: HCV type 2a
- (B) MAP POSITION: position -168 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 2a specific probe HcPr136"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TTRCCGGRRAA GACTGG

16

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 2a (Chan et al., 1992)

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: HCV type 2a
- (B) MAP POSITION: Position -117 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 2a specific probe HcPr137"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

TGRCCGGGCA TAGAGT

16

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HCV type 2b (Nakao et al., 1991)

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: HCV type 2b
- (B) MAP POSITION: position -168 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 2b specific probe HcPr126"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TTACCGGGAA GACTGG

16

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: HCV type 2b (Nakao et al., 1991)

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: HCV type 2b
(B) MAP POSITION: position -117 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..16
(D) OTHER INFORMATION: /standard_name= "HCV type 2b specific probe HcPr127"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TGACCGGGACA TAGAGT

16

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: HCV type 3

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: HCV type 3
(B) MAP POSITION: position -170 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 3 specific probe HcPr128"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

AATCGCTGGG GTGACC

16

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HCV type 3

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: HCV type 3
- (B) MAP POSITION: position -117 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 3 specific probe HcPr 129"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TTTCTGGGTA TTGAGC

16

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HCV type 3a (Chan et al., 1992)
 - (viii) POSITION IN GENOME:
 - (A) CHROMOSOME SEGMENT: HCV type 3a
 - (B) MAP POSITION: position -146 of 5' end
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..16
 - (D) OTHER INFORMATION: /standard_name= "HCV type 3a specific probe HcPr140"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
TCTTGGAGCA ACCCGC
- 16
- (2) INFORMATION FOR SEQ ID NO: 16:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HCV type 3b (Chan et al., 1992)
 - (viii) POSITION IN GENOME:
 - (A) CHROMOSOME SEGMENT: HCV type 3b
 - (B) MAP POSITION: position -146 of 5' end
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..16
 - (D) OTHER INFORMATION: /standard_name= "HCV type 3b specific probe HcPr139"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TCTTGAAACA ACCCGC

16

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 4 (Bukh et al.,
1992)

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: HCV type 4
- (B) MAP POSITION: position -170 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type
4 specific probe HcPr 144"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AATYGCCGGG ATGACC

16

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 4

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: HCV type 4

(B) MAP POSITION: position -147 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type 4 specific probe HcPr145"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TTCTTGAAAC TAACCC

16

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 4

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: HCV type 4

(B) MAP POSITION: position -117 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type 4 specific probe HcPr146"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TTTCCGGGCA TTGAGC

16

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV (Kato et al., 1990)

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: HCV

(B) MAP POSITION: position -115 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "Universal HCV probe HcPr 142"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TTGGGCGYGC CCCCCC

16

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 3

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: HCV type 3

(B) MAP POSITION: position -103 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 3 specific probe HcPr 154"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CCGCGAGATC ACTAGC

16

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HCV type 2a (Okamoto et al., 1991)

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: HCV type 2a
- (B) MAP POSITION: position -165 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 2a specific probe HcPr156"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CCGGGAAGAC TGGGTC

16

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 2b (Okamoto et al., 1992)

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: HCV type 2b
(B) MAP POSITION: position - 165 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..16
(D) OTHER INFORMATION: /standard_name= "HCV type 2b specific probe HcPr157"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CCGGAAAGAC TGGGTC

16

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 2a (Okamoto et al., 1991)

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: HCV type 2a
(B) MAP POSITION: position -136 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..16
(D) OTHER INFORMATION: /standard_name= "HCV type 2a specific probe HcPr158"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

ACCCACTCTA TGCCCG

16

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 2b (Okamoto et al., 1992)

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: HCV type 2b
- (B) MAP POSITION: position -136 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 2b specific probe HcPr159"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ACCCACTCTA TGTCCG

16

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 2 (Okamoto et al., 1992)

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: HCV type 2

(B) MAP POSITION: position -126 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type 2 specific probe HcPr160"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

ATAGAGTGGG TTTATC

16

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV (Kato et al., 1990)

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: HCV

(B) MAP POSITION: Position -195 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "Universal HCV probe HcPr153"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TCTGCGGAAC CGGTGA

16

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

AATTGCCAGG AYGACC

16

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GCTCAGTGCC TGGAGA

16

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CCGCGAGACY GCTAGC

16

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CCCCGCAAGA CTGCTA

16

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CGTACAGCCT CCAGGC

16

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GGACCCAGTC TTCCTG

16

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TGCCTGGTCA TTTGGG

16

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

TKTCTGGGTA TTGAGC

16

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

CCGCAAGATC ACTAGC

16

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GAGTGTTGTA CAGCCT

16

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

AATCGCCGGG ATGACC

16

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GAGTGTTGTG CAGCCT

16

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

AATCGCCGGG ACGACC

16

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

AATGCCCGGC AATTTG

16

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

AATCGCCGAG ATGACC

16

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

AATGCTCGGA AATTTG

16

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GAGTGTCGAA CAGCCT

16

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

AATTGCCGGG ATGACC

16

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

TCTCCGGGCA TTGAGC

16

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

AATTGCCGGG ACGACC

16

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

GGGTCCCTTTC CATTGG

16

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

AATCGCCAGG ATGACC

16

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

TGCCTGGAAA TTTGGG

16

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GAGTGTGCGTA CAGCCT

16

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

AGTYCACCGG AATCGC

16

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGAATCGCCA GGACGA

16

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

GAATCGCCGG GTTGAC

16

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: jp62

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GAGTGTGTA CAGCCTCCAG GCCCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	80
CGGGAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG	120
CCCGGCCATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGCGTTGG GTTGCAGA	177

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: gb81

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

GAGTGTGTA CAGCCTCCAG GCCCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGGGAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG	120
CCCGGTCATT TGGGCGTGCC CCCGCAAGAC CGCTAGCCGA	160
GTAGCGTTGG GTTGCAGA	177

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: br56

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

GAGTGTCTGTG CAGCCTCCAG GCCCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA	120
CCCAGAAATT TGGGCCTGCC CCCGCGAGAT CACTAGCCGA	160
GTAGTGTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: bu79

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5'untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GAGTGTGTGA CAGCCTCCAG GCCCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGGGACGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG	120
CCCGGAAATT TGGGCCTGCC CCCGCGAGAC TGCTAGCCGA	160
GTAGTGTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: bu74

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GAGTGTTGTG CAGCCTCCAG GACCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTCCA CCGGAATCGC	80
CGGGATGACC GGGTCCTTTC TTGGAACTAA CCCGCTCAAT	120
GCCCCGAAAT TTGGGCGTGC CCCCCGCGAGA CTGCTAGCCG	160
AGTAGTGTG GGTGCGGA	178

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb80

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GAGTGTGCGTG CAGCCTCCAG GCCCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGGGATGACC GGGTCCTTTC TTGGAACTAA CCCGCTCAAT	120

GCCCCGAAAT TTGGGCGTGC CCCCGCGAGA CTGCTAGCCG	160
AGTAGTGTTG GGTCGCGA	178

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: be82 (also referred to as be99)

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GAGTGTCTGTG CAGCCTCCAG GACCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	80
CAGGACGACC GGGTCCTTTC TTGGATCAAC CCGCTCAATG	120
CCTGGAGATT TGGGCGTGCC CCCGCGAGAC CGCTAGCCGA	160
GTAGTGTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: be90

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

GAGTGTCTGTG CAGCCTCCAG GATCCCCCT CCCGGGAGAG	40
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CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	80
CAGGATGACC GGGTCCTTTC TTGGATTAAC CCGCTCAGTG	120
CCTGGAGATT TGGGCGTGCC CCCGCGAGAC TGCTAGCCGA	160
GTAGTGTGTTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: be91

(viii) POSITION IN GENOME:

- (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GAGTGTGCGTA CAGCCTCCAG GCCCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	80
CGGAAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG	120
TCCGGTCATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCTA	160
GTAGCGTTGG GTTGCAGA	177

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: be92

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GAGTGTCTGA CAGCCTCCAG GCCCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	80
CAGGAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG	120
CCTGGTCATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGCGTTGG GTTGCAGA	177

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: be93

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GAGTGTCTGT CAGCCTCCAG GCCCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA	120
CCCAGACATT TGGGCGTGCC CCCGCGAGAT CACTAGCCGA	160
GTAGTGTGGT GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: be94

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GAGTGTCTGTG CAGCCTCCAG GCCCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA	120
CCCAGACATT TGGGCGTGCC CCCGCAAGAT CACTAGCCGA	160
GTAGTGTGTTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: gb48

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GAGTGTGTA CAGCCTCCAG GACCCCCCTT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGGGATGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG	120
CCCGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGTGTGTTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: gb116

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

GAGTGTGTA CAGCCTCCAG GACCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGGGATGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG	120
CCCGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGTGTGTTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: gb569

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GAGTGTGTA CAGCCTCCAG GACCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGGGATGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG	120

CCCGGAAATT TGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGTGTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: gb358

(viii) POSITION IN GENOME:

- (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

GAGTGTGTA CAGCCTCCAG GACCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGGGATGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG	120
CCCGGAAATT TGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGTGTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: gb549

(viii) POSITION IN GENOME:

- (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

GAGTGTGTCAGCCTCCAG GACCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTTCA CCGGAATCGC	80
CGGGACGACC GGGTCCTTTC TTGGAACAAA CCCGCTCAAT	120
GCCCGGCAAT TTGGCGTGCG CCCCAGAAGA CTGCTAGCCG	160
AGTAGTGTGCGA	178

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
(B) CLONE: cam600
- (viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

GAGTGTGTA CAGCCTCCAG GACCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGAGATGACC GGGTCCTTTC TTGGATCAAC CCGCTCAATG	120
CTCGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCG	160
GTAGTGTGCGA	177

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: cam736

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

GAGTGTGTA CAGCCTCCAG GACCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGAGATGACC GGGTCCTTTC TTGGATCAAC CCGCTCAATG	120
CTCGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGTGTGGA GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: gb809

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

GAGTGTGTA CAGCCTCCAG GACCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGAGATGACC GGGTCCTTTC TTGGATCAAC CCGCTCAATG	120
CTCGGAAATT TGGGCGTGCC CCCGCAAGAC CGCTAGCCGA	160
GTAGTGTGGA GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb487

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GAGTGTGTA CAGCCTCCAG GACCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CAGGATGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG	120
CCTGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGTGTGGA GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb724

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

GAGTGTGTA CAGCCTCCAG GACCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTTCA CCGGAATCGC	80
CAGGACGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG	120
CCTGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGTGTGGA GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: be97

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GAGTGTGTA CAGCCTCCAG GACCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CAGGACGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG	120
CCTGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGTGTGGA GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: be95

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

GAGTGTGAA CAGCCTCCAG GACCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	80
CGGGATGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG	120

CCCGGAGATT TGGCGTGCC CCCGCGAGAC TGCTAGCCGA	160
GTAGTGTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: be96

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

GAGTGTGAA CAGCCTCCAG GACCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	80
CGGGACGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG	120
CCCGGAGATT TGGCGTGCC CCCGCGAGAC TGCTAGCCGA	160
GTAGTGTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: be98

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

GAGTGTCTGTG CAGCCTCCAG GACCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGGGTTGACC GGGTCCTTTC TTGGAACTAC CCGCTCAATG	120
CCCGGAAATT TGGGCGTGCC CCCGCGAGAC TGCTAGCCGA	160
GTAGTGTGTTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: gb438

(viii) POSITION IN GENOME:

- (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

GAGTGTCTGAA CAGCCTCCAG GATCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTTCA CCGGAATCGC	80
CGGGATGACC GGGTCCTTTC TTGGAATCAA CCCGCTCAAT	120
GCCCCGAAAT TTGGGCGTGC CCCCGCGAGA CTGCTAGCCG	160
AGTAGTGTGTTGG GTCGCGA	178

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
(B) CLONE: be90

(viii) POSITION IN GENOME:
(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu
1 5 10
Ser Ile Tyr Gln Cys Cys Asp Leu Ala Pro Glu Ala
15 20
Arg Gln Ala Ile Lys Ser Leu Thr Glu Arg Leu Tyr
25 30 35
Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu
50 55 60
Thr Thr Ser Cys Gly Asn Thr Leu Thr Cys Tyr Leu
65 70
Lys Ala Ser Ala Ala Cys Arg Ala Ala Lys Leu Gln
75 80
Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala
100 105
Ala Ser Leu Arg Val
110

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
(B) CLONE: be91

(viii) POSITION IN GENOME:
(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu
1 5 10
Ser Ile Tyr Gln Ala Cys Ser Leu Pro Gln Glu Ala
15 20

Arg Thr Val Ile His Ser Leu Thr Glu Arg Leu Tyr
25 30 35
Val Gly Gly Pro Met Ile Asn Ser Lys Gly Gln Ser
40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe
50 55 60
Thr Thr Ser Met Gly Asn Thr Met Thr Cys Tyr Ile
65 70
Lys Ala Leu Ala Ala Cys Lys Ala Ala Gly Ile Val
75 80
Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu
100 105
Arg Asn Leu Arg Ala
110

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
(B) CLONE: be92

(viii) POSITION IN GENOME:
(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu
1 5 10
Ser Ile Tyr Leu Ala Cys Ser Leu Pro Glu Gln Ala
15 20
Arg Thr Ala Ile His Ser Leu Thr Glu Arg Leu Tyr
25 30 35
Val Gly Gly Pro Met Leu Asn Ser Lys Gly Gln Thr
40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe
50 55 60
Thr Thr Ser Met Gly Asn Thr Ile Thr Cys Tyr Val
65 70
Lys Ala Gln Ala Ala Cys Lys Ala Ala Gly Ile Ile
75 80
Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu
100 105
Arg Asn Leu Arg Ala
110

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: be93

(viii) POSITION IN GENOME:

(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu
1 5 10
Glu Ile Tyr Gln Cys Cys Asn Leu Glu Pro Glu Ala
15 20
Arg Lys Val Ile Ser Ser Leu Thr Glu Arg Leu Tyr
25 30 35
Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Ala Gln
40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu
50 55 60
Pro Thr Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile
65 70
Lys Ala Thr Thr Ala Ala Lys Ala Ala Gly Leu Arg
75 80
Asn Pro Asp Phe Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg
100 105
Ala Ala Leu Arg Ala
110

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb48

(viii) POSITION IN GENOME:

(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu
1 5 10
Glu Val Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala
15 20
Arg Lys Ala Ile Thr Ala Leu Thr Glu Arg Leu Tyr
25 30 35
Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr
50 55 60
Thr Thr Ser Phe Gly Asn Thr Leu Thr Cys Tyr Leu
65 70
Lys Ala Ser Ala Ala Ile Lys Ala Ala Gly Leu Arg
75 80
Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys
100 105
Arg Pro Leu Gly Ala
110

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb116

(viii) POSITION IN GENOME:

(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu
1 5 10

Glu Val Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala
15 20
Arg Arg Ala Ile Thr Ala Leu Thr Glu Arg Leu Tyr
25 30 35
Val Gly Gly Pro Met His Asn Ser Arg Gly Asp Leu
40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr
50 55 60
Thr Thr Ser Phe Gly Asn Thr Leu Thr Cys Tyr Leu
65 70
Lys Ala Ser Ala Ala Ile Arg Ala Ala Gly Leu Arg
75 80
Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys
100 105
Arg Ala Leu Gly Ala
110

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: gb215

(viii) POSITION IN GENOME:

- (B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu
1 5 10
Glu Val Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala
15 20
Arg Lys Val Ile Thr Ala Leu Thr Glu Arg Leu Tyr
25 30 35
Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr
50 55 60
Thr Thr Ser Phe Gly Asn Thr Leu Thr Cys Tyr Leu
65 70
Lys Ala Ser Ala Ala Ile Arg Ala Ser Gly Leu Arg
75 80

Asp Cys Thr Met Leu Val Tyr Gly Asp Asp Leu Val
85 90 95
Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys
100 105
Arg Ala Leu Gly Val
110

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: gb358

(viii) POSITION IN GENOME:

- (B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu
1 5 10
Glu Val Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala
15 20
Arg Lys Ala Ile Thr Ala Leu Thr Glu Arg Leu Tyr
25 30 35
Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr
50 55 60
Thr Thr Ser Phe Gly Asn Thr Leu Thr Cys Tyr Leu
65 70
Lys Ala Ser Ala Ala Ile Arg Ala Ala Gly Leu Arg
75 80
Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys
100 105
Arg Ala Leu Gly Ala
110

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
(B) CLONE: gb549

(viii) POSITION IN GENOME:
(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu.
1 5 10
Glu Ile Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala
15 20
Arg Lys Val Ile Ser Ala Leu Thr Glu Arg Leu Tyr
25 30 35
Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu
40 45
Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr
50 55 60
Thr Thr Ser Phe Gly Asn Thr Val Thr Cys Tyr Leu
65 70
Lys Ala Val Ala Ala Thr Arg Ala Ala Gly Leu Lys
75 80
Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala
100 105
Arg Ala Leu Arg Ala
110

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: gb809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Ser Thr Val Thr Glu Arg Asp Ile Lys Val Glu Glu
1 5 10
Glu Val Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala
15 20
Arg Lys Val Ile Ala Ala Leu Thr Glu Arg Leu Tyr
25 30 35
Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr
50 55 60
Thr Thr Ser Phe Gly Asn Thr Met Thr Cys Tyr Leu
65 70
Lys Ala Ser Ala Ala Ile Arg Ala Ala Gly Leu Lys
75 80
Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys
100 105
Arg Ala Leu Gly Ala
110

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: be95

(viii) POSITION IN GENOME:

- (B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu
1 5 10
Ser Ile Tyr Gln Ser Cys Asp Leu Gln Pro Glu Ala
15 20
Arg Ala Ala Ile Arg Ser Leu Thr Gln Arg Leu Tyr
25 30 35
Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Gln
40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe
50 55 60

Thr Thr Ser Met Gly Asn Thr Met Thr Cys Tyr Ile
65 70
Lys Ala Leu Ala Ser Cys Arg Ala Ala Arg Leu Arg
75 80
Asp Cys Thr Leu Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu
100 105
Ala Ser Leu Arg Ala
110

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GAGTGTTGTA CAGCCTCC

18

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

TGCCCGGAAA TTTGGGC

17

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

TGCCCGGAGA TTTGGG

16

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

GAGTGTGGAA CAGCCTC

17

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

GGGGGCCTGG AGGCTG

16